



SEQUENCE LISTING

<110> LITTLE, MELVYN
KIPRIYANOV, SERGEY
MOLDENHAUER, GERHARD
DEUTSCHES KREBSFORSCHUNGSZEUTRUM

<120> MUTATED OKT3 ATIBODY

<130> 035280047US00

<140> 09/424,705

<141> 2000-06-02

<150> PCT/DE98/01409

<151> 1998-05-22

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<170> FastSEQ for Windows Version 4.0

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<211> 909

<212> DNA

<213> Homo sapiens

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<221> CDS

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gct ggc ttg ctg ctg ctg gca gct cag ccg gcc atg gcg cag gtg cag 102
Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln
10 15 20 25

ctg cag cag tct ggg gct gaa ctg gca aga cct ggg gcc tca gtg aag 150
Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys
30 35 40

atg tcc tgc aag gct tct ggc tac acc ttt act agg tac acg atg cac 198
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
45 50 55

tgg gta aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att 246
Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
60 65 70

aat cct agc cgt ggt tat act aat tac aat cag aag ttc aag gac aag 294
Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys
75 80 85

gcc aca ttg act aca gac aaa tcc tcc agc aca gcc tac atg caa ctg	342
Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu	
90 95 100 105	
agc agc ctg aca tct gag gac tct gca gtc tat tac tgt gca aga tat	390
Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr	
110 115 120	
tat gat gat cat tac agc ctt gac tac tgg ggc caa ggc acc act ctc	438
Tyr Asp Asp His Tyr Ser Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu	
125 130 135	
aca gtc tcc tca gcc aaa aca aca ccc aag ctt gaa gaa ggt gaa ttt	486
Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu Glu Glu Gly Glu Phe	
140 145 150	
tca gaa gca cgc gta gat atc gtg ctc act cag tct cca gca atc atg	534
Ser Glu Ala Arg Val Asp Ile Val Leu Thr Gln Ser Pro Ala Ile Met	
155 160 165	
tct gca tct cca ggg gag aag gtc acc atg acc tgc agt gcc agc tca	582
Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser	
170 175 180 185	
agt gta agt tac atg aac tgg tac cag cag aag tca ggc acc tcc ccc	630
Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro	
190 195 200	
aaa aga tgg att tat gac aca tcc aaa ctg gct tct gga gtc cct gct	678
Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala	
205 210 215	
cac ttc agg ggc agt ggg tct ggg acc tct tac tct ctc aca atc agc	726
His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser	
220 225 230	
ggc atg gag gct gaa gat gct gcc act tat tac tgc cag cag tgg agt	774
Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser	
235 240 245	
agt aac cca ttc acg ttc ggc tcg ggg aca aag ttg gaa ata aac cgg	822
Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn Arg	
250 255 260 265	
gct gat act gca cca act gga tcc gaa caa aag ctg atc tca gaa gaa	870
Ala Asp Thr Ala Pro Thr Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu	
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 Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
 35 40 45
 Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
 50 55 60
 Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
 65 70 75 80
 Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys
 85 90 95
 Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
 100 105 110
 Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser Leu
 115 120 125
 Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr
 130 135 140
 Thr Pro Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg Val Asp Ile
 145 150 155 160
 Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys
 165 170 175
 Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
 180 185 190
 Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr
 195 200 205
 Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser
 210 215 220
 Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala
 225 230 235 240
 Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly
 245 250 255
 Ser Gly Thr Lys Leu Glu Ile Asn Arg Ala Asp Thr Ala Pro Thr Gly
 260 265 270
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 His His His
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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (28) ... (897)

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 Met Lys Tyr Leu Leu Pro Thr Ala Ala
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gct ggc ttg ctg ctg ctg gca gct cag ccg gcc atg gcg cag gtg cag 102
 Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln

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ctg cag cag tct ggg gct gaa ctg gca aga cct ggg gcc tca gtg aag				150
Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys	30	35	40	
atg tcc tgc aag gct tct ggc tac acc ttt act agg tac acg atg cac				198
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His	45	50	55	
tgg gta aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att				246
Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile	60	65	70	
aat cct agc cgt ggt tat act aat tac aat cag aag ttc aag gac aag				294
Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys	75	80	85	
gac aag gcc aca ttg act aca gac aaa tcc tcc agc aca gcc tac atg				342
Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met	90	95	100	105
caa ctg agc agc ctg aca tct gag gac tct gca gtc tat tac tgt gca				390
Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala	110	115	120	
aga tat tat gat gat cat tac agc ctt gac tac tgg ggc caa ggc acc				438
Arg Tyr Tyr Asp Asp His Tyr Ser Leu Asp Tyr Trp Gly Gln Gly Thr	125	130	135	
act ctc aca gtc tcc tca gcc aaa aca aca ccc aag ctt ggc ggt gat				486
Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu Gly Gly Asp	140	145	150	
atc ttg ctc acc caa act cca gct tct ttg gct gtg tct cta ggg cag				534
Ile Leu Leu Thr Gln Thr Pro Ala Ser Leu Ala Val Ser Leu Gly Gln	155	160	165	
agg gcc acc atc tcc tgc aag gcc agc caa agt gtt gat tat gat ggt				582
Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly	170	175	180	185
gat agt tat ttg aac tgg tac caa cag att cca gga cag cca ccc aaa				630
Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys	190	195	200	
ctc ctc atc tat gat gca tcc aat cta gtt tct ggg atc cca ccc agg				678
Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg	205	210	215	
ttt agt ggc agt ggg tct ggg aca gac ttc acc ctc aac atc cat cct				726
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro	220	225	230	
gtg gag aag gtg gat gct gca acc tat cac tgt cag caa agt act gag				774
Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu	235	240	245	

gat ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa cgg gct 822
 Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala
 250 255 260 265

gat gct gcg gcc gct gga tcc gaa caa aag ctg atc tca gaa gaa gac 870
 Asp Ala Ala Ala Ala Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp
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 Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
 35 40 45
 Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
 50 55 60
 Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
 65 70 75 80
 Asn Tyr Asn Gln Lys Phe Lys Asp Lys Asp Lys Ala Thr Leu Thr Thr
 85 90 95
 Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser
 100 105 110
 Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr
 115 120 125
 Ser Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala
 130 135 140
 Lys Thr Thr Pro Lys Leu Gly Gly Asp Ile Leu Leu Thr Gln Thr Pro
 145 150 155 160
 Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
 165 170 175
 Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr
 180 185 190
 Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser
 195 200 205
 Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly
 210 215 220
 Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala
 225 230 235 240
 Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly
 245 250 255
 Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Ala Ala Gly Ser
 260 265 270
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser His His His His
 275 280 285
 His His

Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser
170 175 180 185

tac atg aac tgg tac cag cag aag tca ggc acc tcc ccc aaa aga tgg 630
Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp
190 195 200

att tat gac aca tcc aaa ctg gct tct gga gtc cct gct cac ttc agg 678
Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg
205 210 215

ggc agt ggg tct ggg acc tct tac tct ctc aca atc agc ggc atg gag 726
Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu
220 225 230

gct gaa gat gct gcc act tat tac tgc cag cag tgg agt agt aac cca 774
Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
235 240 245

ttc acg ttc ggc tcg ggg aca aag ttg gaa ata aac cgg gct gat act 822
Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn Arg Ala Asp Thr
250 255 260 265

gca cca act gga tcc gaa caa aag ctg atc tca gaa gaa gac cta aac 870
Ala Pro Thr Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
270 275 280

tca cat cac cat cac cat cac taatctaga 900
Ser His His His His His His
285

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35 40 45
Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly
50 55 60
Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr
65 70 75 80
Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu
85 90 95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp
100 105 110
Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg
115 120 125
Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val
130 135 140
Ser Ser Ala Lys Thr Thr Pro Lys Leu Gly Gly Asp Ile Val Leu Thr

145					150					155				160	
Gln	Ser	Pro	Ala	Ile	Met	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met
				165					170					175	
Thr	Cys	Ser	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln
			180					185					190		
Lys	Ser	Gly	Thr	Ser	Pro	Lys	Arg	Trp	Ile	Tyr	Asp	Thr	Ser	Lys	Leu
		195					200				205				
Ala	Ser	Gly	Val	Pro	Ala	His	Phe	Arg	Gly	Ser	Gly	Ser	Gly	Thr	Ser
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Tyr	Ser	Leu	Thr	Ile	Ser	Gly	Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr
225					230					235				240	
Tyr	Cys	Gln	Gln	Trp	Ser	Ser	Asn	Pro	Phe	Thr	Phe	Gly	Ser	Gly	Thr
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Lys	Leu	Glu	Ile	Asn	Arg	Ala	Asp	Thr	Ala	Pro	Thr	Gly	Ser	Glu	Gln
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 <213> Homo sapiens

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